Amendments to the Claims

1-26. (Canceled).

27. (Currently amended) A method for separating ligands from a sample and recovering a modified sample for analysis of remaining components ~~ligands~~ comprising:

removing at least two specific predefined ligands from the sample, so that a plurality of components remains in the sample following removal of the at least two specific predefined ligands, thereby producing a modified sample comprising a plurality of components to be analyzed; and

recovering the modified sample ~~analyzing the remaining ligands in the sample~~.

28. (Previously presented) The method of claim 27 wherein at least three ligands are removed.

29. (Previously presented) The method of claim 28 wherein at least four ligands are removed.

30. (Currently amended) The method of claim 27 wherein the ligands and components are proteins.

31. (Currently amended) The method of claim 27 wherein the ligands are removed by binding to specific predefined receptors wherein the receptors are in insoluble form or are ~~is~~ insolubilized after binding to the ligands

32. (Currently amended) The method of claim 27 wherein at least 50% by weight of all proteins ~~ligands~~ in the sample are removed.

33. (Currently amended) The method of claim 32 wherein at least 75% by weight of all proteins ~~ligands~~ in the sample are removed.

34. (Previously presented) The method of claim 31 further comprising, removing the bound ligands from the receptors.

35. (Currently amended) The method of claim 34 ~~33~~ further comprising, repeating the method ~~process~~ by reusing the receptors with a new sample.

36. (Currently amended) The method of claim 35 ~~34~~ wherein the method ~~process~~ is repeated 20 times with the same receptors.

37. (Currently amended) The method of claim 35 wherein the method ~~process~~ is repeated 50 times with the same receptors.

38. (Currently amended) The method of claim 36 wherein the method ~~process~~ is repeated 200 times with the same receptors.

39. (Currently amended) The method of claim 27, further comprising the step of analyzing remaining components in the modified sample ~~wherein the remaining ligands are analyzed~~ by separation and quantification of the remaining components ~~ligands~~.

40. (Previously presented) The method of claim 31 wherein at least one immobilized receptor is selectively removable from at least one other immobilized receptor.

41. (Currently amended) The method of claim 42 ~~31~~ wherein one ~~division of~~ receptor is selectively removable from another ~~division of~~ receptor.

42. (Currently amended) The method of claim 31 wherein ~~at least two divisions of~~ receptors having first and second binding specificities are immobilized in at least two predefined locations, wherein at least one receptor having a first binding specificity is located in a different predefined location from another receptor having a second binding specificity, and wherein the sample is sequentially passed through both predefined locations.

43. (Canceled).

44. (Currently amended) The modified ~~ligand-containing~~ sample produced by the method ~~process~~ of claim 27.

45. (New) The method of claim 27, further comprising the step of analyzing at least one component remaining in the modified sample.

46. (New) The method of claim 45, wherein the analyzing step comprises determining a physical characteristic of at least one component.

47. (New) The method of claim 46, wherein the physical characteristic is selected from the group consisting of molecular weight, charge, mass to charge ratio, and isoelectric point.

48. (New) The method of claim 45, wherein the analyzing step comprises performing mass spectrometry, 2D gel electrophoresis, chromatography, an immunoassay, a binding assay, or any combination of the foregoing.

49. (New) The method of claim 45, wherein the analyzing step comprises identifying the component.

50. (New) The method of claim 45, wherein the analyzing step comprises determining the presence, abundance, or both, of the component.

51. (New) The method of claim 45, wherein the presence, abundance, or both, of the component in the sample, was unknown prior to the analyzing step.

52. (New) The method of claim 27, further comprising the step of analyzing a plurality of components remaining in the modified sample.

53. (New) The method of claim 52, wherein the analyzing step comprises determining a physical characteristic of a plurality of components.

54. (New) The method of claim 52, wherein the physical characteristic is selected from the group consisting of molecular weight, charge, mass to charge ratio, and isoelectric point

55. (New) The method of claim 52, wherein the analyzing step comprises performing mass spectrometry, 2D gel electrophoresis, chromatography, an immunoassay, or any combination of the foregoing.

56. (New) The method of claim 52, wherein the analyzing step comprises identifying a plurality of components.

57. (New) The method of claim 52, wherein the analyzing step comprises determining the presence, abundance, or both, of a plurality of components.

58. (New) The method of claim 52, wherein the presence, abundance, or both, of the components in the sample, was unknown prior to the analyzing step.

59. (New) The method of claim 27, wherein the specific predefined receptors were selected to facilitate analysis of ligands remaining in the modified sample.

60. (New) The method of claim 27, further comprising concentrating components remaining in the modified sample, adding a buffer to the modified sample, dialyzing the modified sample, lyophilizing the modified sample, or any combination of the foregoing.

61. (New) The method of claim 27, wherein the modified sample has improved characteristics for analysis of components remaining in the sample.

62. (New) The method of claim 27, wherein at least one of the specific predefined ligands is present at higher abundance than at least one of the plurality of components remaining in the sample after removal of the specific predefined ligands.

63. (New) The method of claim 27, wherein the removing step comprises contacting the sample with an affinity binding composition comprising:

a first and second solid phase matrix contacting each other;

a first receptor immobilized on said first solid phase matrix, capable of specific binding to a first ligand but not a second ligand; and

a second receptor immobilized on said second solid phase matrix, capable of specific binding to the second ligand but not the first ligand.

64. (New) The method of claim 63, wherein the affinity binding composition further comprises:

a third receptor immobilized on a third solid phase matrix, capable of specific binding to a third ligand but not the first ligand or the second ligand.

65. (New) The method of claim 64, wherein the third solid phase matrix contacts the first and second solid phase matrices.

66. (New) The method of claim 63, wherein the affinity binding composition further comprises:

a fourth receptor immobilized on a fourth solid phase matrix, capable of specific binding to a fourth ligand but not the first ligand, the second ligand or the third ligand.

67. (New) The method of claim 66, wherein the fourth solid phase matrix contacts the first, second, and third solid phase matrices.

68. (New) The method of claim 67, wherein the affinity binding composition further comprises:

a fifth receptor immobilized on a fifth solid phase matrix, capable of specific binding to a fifth ligand but not the first ligand, the second ligand, the third ligand or the fourth ligand.

69. (New) The method of claim 68, wherein the fifth solid phase matrix contacts the first, second, third, and fourth solid phase matrices.

70. (New) The method of claim 63, wherein the sample is passed through a column containing the affinity binding composition.

71. (New) The method of claim 63, wherein each solid phase matrix comprises a plurality of particles.

72. (New) The method of claim 71, wherein the particles are present as a mixture.

73. (New) The method of claim 63, wherein the first receptor is not immobilized on the second solid phase matrix.

74. (New) The method of claim 63, wherein the receptors are antibodies, antibody fragments, or lectins.

75. (New) The method of claim 63, wherein the receptors are recombinantly produced.

76. (New) The method of claim 63, wherein at least one receptor is selected from the group consisting of metals, cofactors, nucleic acids, aptamers, combinatorial compounds, combinatorial peptides, combinatorial oligomers and combinatorial polymers.

77. (New) The method of claim 27, wherein the removing step comprises contacting the sample with an affinity binding composition comprising:

a plurality of solid phase matrices arranged such that each solid phase matrix is in contact with at least one other solid phase matrix; and

a plurality of receptors, the plurality of receptors comprising receptors of a plurality of receptor types, wherein the receptors are immobilized on the plurality of solid phase matrices such that each receptor type is immobilized on a single matrix and each receptor type binds specifically to a different ligand.

78. (New) The method of claim 77, wherein each solid phase matrix comprises a plurality of particles.

79. (New) The method of claim 77, wherein the particles are present as a mixture.

80. (New) The method of claim 77, wherein the receptors are antibodies, antibody fragments, or lectins.

81. (New) The method of claim 77, wherein the receptors are recombinantly produced.

82. (New) The method of claim 77, wherein at least one receptor is selected from the group consisting of metals, cofactors, nucleic acids, aptamers, combinatorial compounds, combinatorial peptides, combinatorial oligomers and combinatorial polymers.

83. (New) The method of claim 77 wherein the sample is passed through a column containing the affinity binding composition.

84. (New) The method of claim 27, wherein the removing step comprises contacting the sample with an affinity binding composition comprising:

a plurality of solid phase matrices arranged such that each solid phase matrix is in contact with at least one other solid phase matrix; and

a plurality of receptors having different ligand binding specificities, wherein the receptors are immobilized on the plurality of solid phase matrices such that each solid phase matrix has a different ligand binding specificity.

85. (New) The method of claim 84, wherein the sample is passed through a column containing the affinity binding composition.

86. (New) The method of claim 84, wherein each solid phase matrix comprises a plurality of particles.

87. (New) The method of claim 84, wherein the particles are present as a mixture.

88. (New) The method of claim 84, wherein the receptors are antibodies, antibody fragments, or lectins.

89. (New) The method of claim 84, wherein the receptors are recombinantly produced.

90. (New) The method of claim 84, wherein at least one receptor is selected from the group consisting of metals, cofactors, nucleic acids, aptamers, combinatorial compounds, combinatorial peptides, combinatorial oligomers and combinatorial polymers.

91. (New) The method of claim 27, wherein the removing step comprises passing the sample through first and second solid phase matrices, the first and second solid phase matrices having different ligand binding specificities and being arranged in layers.

92. (New) The method of claim 91, wherein the solid phase matrices are in an affinity column.

93. (New) The method of claim 91, wherein the solid phase matrices each comprises a plurality of particles.

94. (New) The method of claim 91, wherein the receptors are antibodies, antibody fragments, or lectins.

95. (New) The method of claim 91, wherein the receptors are recombinantly produced.

96. (New) The method of claim 91, wherein at least one receptor is selected from the group consisting of metals, cofactors, nucleic acids, aptamers, combinatorial compounds, combinatorial peptides, combinatorial oligomers and combinatorial polymers.

97. (New) The method of claim 27, wherein the removing step comprises passing the sample through first and second solid phase matrices, wherein the first and second solid phase matrices are separated by a permeable membrane.

98. (New) A method for separating ligands from a sample and analyzing remaining components comprising:

providing a sample comprising at least two specific predefined ligands and one or more additional components;

removing at least two of the specific predefined ligands from the sample; and

analyzing at least 100 components remaining in the sample.

99. (New) A method for separating ligands from a sample and analyzing remaining components comprising:

providing a sample comprising at least two specific predefined ligands and one or more additional components;

removing at least two of the specific predefined ligands from the sample; and

analyzing components remaining in the sample by 2D gel electrophoresis, mass spectrometry, chromatography, an immunoassay, or any combination of the foregoing.

100. (New) A method for separating ligands from a sample for analysis of remaining ligands comprising:

providing a sample comprising at least two specific predefined ligands and a plurality of additional components to be analyzed; and

removing a plurality of the specific predefined ligands from the sample, thereby producing a modified sample, wherein removal of the plurality of specific predefined ligands renders at least one remaining component detectable by a detection method that was unable to detect the component prior to removal of the plurality of specific predefined ligands.

101. (New) The method of claim 100, wherein removal of the plurality of specific predefined ligands allows quantitation of at least 50% more components in the modified sample than could be quantitated in the sample containing the plurality of specific predefined ligands.

102. (New) The method of claim 100, further comprising the step of analyzing at least one component remaining in the modified sample.

103. (New) The method of claim 32 wherein at least 90% by weight of all proteins in the sample are removed.

104. (New) The method of claim 27, wherein at least one of the specific predefined ligands is selected from the group consisting of: one or more immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein A1, α_2-macroglobulin, fibrinogen, and prealbumin.

105. (New) The method of claim 27, wherein at least two of the specific predefined ligands are selected from the group consisting of: one or more immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein A1, α_2-macroglobulin, fibrinogen, and prealbumin.

106. (New) The method of claim 27, wherein at least three of the specific predefined ligands are selected from the group consisting of: one or more immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein A1, α_2-macroglobulin, fibrinogen, and prealbumin.

107. (New) The method of claim 27, wherein at least four of the specific predefined ligands are selected from the group consisting of: one or more immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein A1, α_2-macroglobulin, fibrinogen, and prealbumin.

108. (New) The method of claim 27, further comprising the step of: subjecting the sample to deglycosylation.

109. (New) The method of claim 27, further comprising the step of: subjecting the modified sample to deglycosylation.

WHAT IS CLAIMED IS:

1. A method comprising sequentially contacting a sample with at least a first stationary phase and a second stationary phase under chromatographic conditions, wherein the specificity of said first stationary phase for at least one constituent present in said sample is at least uncertain, and the specificity of said second stationary phase for said at least one constituent is certain, to at least determine the binding identity of said at least one constituent.

2. The method of Claim 1, wherein said method is a method of evaluating the specificity of said first stationary phase for said at least one constituent present in said sample.

3. The method of Claim 2, wherein said sample is contacted with said first stationary phase and then said second stationary phase.

4. The method of Claim 3, wherein said method further comprises:

(a) contacting said sample with said first stationary phase to bind a fraction of said sample that comprises said at least one constituent;

(b) separating said binding fraction from said first stationary phase; and

(c) contacting said binding fraction with said second stationary phase.

5. The method of Claim 3, wherein said first stationary phase comprises a pharmaceutical agent and said method is a method of determining the specificity of said pharmaceutical agent for said at least one constituent present in said sample.

6. The method of Claim 1, further comprising analyzing any constituents that did not bind to said second stationary phase.

7. The method of Claim 6, wherein said analyzing comprises using at least one of: one dimensional gel electrophoresis, two dimensional gel electrophoresis, matrix assisted laser desorption/ionization mass spectroscopy, liquid chromatography/mass spectroscopy,

biomolecular interaction, immunochemical analysis, nuclear magnetic resonance and circular dichroism.

8. The method of Claim 1, wherein said method is a method of determining the specificity of a pharmaceutical agent for at least one constituent present in said sample.

9. The method of Claim 8, wherein said sample is contacted with said second stationary phase first and said first stationary phase second.

10. The method of Claim 9, wherein said method further comprises:

(a) contacting said sample with said second stationary phase to bind a fraction of said sample that comprises at least one constituent;

(b) separating said binding fraction from said second stationary phase; and

(c) contacting said binding fraction with said first stationary phase.

11. The method of Claim 9, wherein said first stationary phase comprises said pharmaceutical agent.

12. The method of Claim 10, further comprising analyzing any constituents that did not bind to said first stationary phase.

13. The method of Claim 12, wherein said analyzing comprises performing at least one of: one dimensional gel electrophoresis, two dimensional gel electrophoresis, matrix assisted laser desorption/ionization mass spectroscopy, liquid chromatography/mass spectroscopy, biomolecular interaction, immunochemical analysis, nuclear magnetic resonance and circular dichroism.

14. The method of Claim 1, wherein said sample comprises a population of proteins and said method is a method of separating a sub-population of proteins from said population of proteins.

15. The method of Claim 14, wherein said separating comprises:

(a) contacting said sample comprising a class of proteins with said first stationary phase to bind a fraction of said sample that comprises said population of proteins;

(b) collecting said binding fraction from said first stationary phase; and

(c) contacting said binding fraction with said second stationary phase so that said sub-population of proteins binds to said second stationary phase and any remaining members of said population do not bind to said second stationary phase.

16. The method of Claim 1, wherein said first and second stationary phases comprise ligands chosen from: antibodies or binding fragments thereof, diabodies, minibodies, antigens, dyes, single chain variants, proteins, glycoproteins, peptides, nucleic acids, vitamins, inorganic chemicals and organic chemicals.

17. The method of Claim 16, wherein at least one stationary phase comprises chlorotriazine affinity ligands.

18. The method of Claim 16, wherein at least one stationary phase comprises immunoaffinity ligands.

19. The method of Claim 16, wherein said first stationary phases comprises chlorotriazine affinity ligands and said second stationary phase comprises immunoaffinity ligands.

20. The method of Claim 1, wherein said first and second stationary phases are connected by a conduit.

21. A method of determining the specificity of a pharmaceutical agent for at least one constituent present in said sample comprising sequentially contacting a sample with at least a first stationary phase and a second stationary phase under chromatographic conditions, wherein the specificity of said first stationary phase for at least one constituent present in said sample is at least uncertain, and the specificity of said second stationary phase for said

at least one constituent is certain, to at least determine the binding identity of said at least one constituent.

22. The method of Claim 21, wherein said sample is contacted with said second stationary phase first and said first stationary phase second.

23. The method of Claim 22, wherein said method further comprises:

(a) contacting said sample with said second stationary phase to bind a fraction of said sample that comprises at least one constituent;

(b) separating said non-binding fraction from said second stationary phase; and

(c) contacting said non-binding fraction with said first stationary phase.

24. The method of Claim 22, wherein said first stationary phase comprises said pharmaceutical agent.

25. The method of Claim 23, further comprising analyzing any constituents that did not bind to said first stationary phase.

26. The method of Claim 25, wherein said analyzing comprises performing at least one of: one dimensional gel electrophoresis, two dimensional gel electrophoresis, matrix assisted laser desorption/ionization mass spectroscopy, liquid chromatography/mass spectroscopy, biomolecular interaction, immunochemical analysis, nuclear magnetic resonance and circular dichroism.

27. A method of evaluating the specificity of a stationary phase comprising contacting a sample with at least a first stationary phase and second stationary phase under chromatographic conditions, wherein the specificity of said first stationary phase for at least one constituent present in the sample is at least uncertain, and the specificity of said second stationary phase for said at least one constituent is certain.

28. A method comprising forwarding data representing a result of an analysis step obtained by at least one of the method of Claim 6, the method of Claim 12 and the method of claim 25.

29. The method according to Claim 28, wherein said data is transmitted to a remote location.

30. A method comprising receiving data representing a result of an analysis step obtained by the method of Claim 28.

31. A system comprising:

(a) a sample comprising at least one constituent;

(b) a first stationary phase wherein the specificity for at least one constituent present in said sample in at least uncertain; and

(c) a second stationary phase wherein the specificity for said at least one constituent in certain.

32. The system of Claim 31, wherein at least one of said stationary phases comprises chlorotriazine affinity ligands.

33. A device comprising a first stationary phase of uncertain specificity for at least one constituent of a sample and a second stationary phase of certain specificity for said at least one constituent of a sample.

34. The device of Claim 33, wherein said device is a chromatography column.

35. The device of Claim 33, wherein said device is a microfluidic device.

36. A kit comprising:

(a) a first stationary phase of at least uncertain specificity;

(b) a second stationary phase of certain specificity; and

(c) instructions for using the first and second stationary phases in the method of Claim 1.